

APPENDIX I

Optimal global alignment

Sequence 1: O'Donnell (WO 99/37661) (572 letters)
Sequence 2: US 10/025,222: SEQ. ID NO:2 (599 letters)

Substitution matrix: blosum62
Gap penalty: - (11 + 1 * (gap length))

Score: 2831
Identical: 555/605 (91%), Similar: 560/605 (92%), Gap: 39/605 (6%)

seq1	1	M-----I	IGLCPFHDEKTPSFTVSEDKQICHCF	27
:				
seq2	1	LRIDQSIINEIKDKTDILDLVSEYVKLEKGRNYIGLCPFHDEKTPSFTVSEDKQICHCF		60
seq1	28	GCKKGGNVFQFTQEIKDISFVEAVKELGDRNLNVAVDIEATQSNSNVQIASDDLQMIEMHE		87
:				
seq2	61	GCKKGGNVFQFTQEIKDISFVEAVKELGDRNVNVAVDIEATQSNSNVQIASDDLQMIEMHE		120
seq1	88	LIQEFYYYYALTKTVEGEQALTYLQERGFTHALIKERGIGFAPDSSHCHDFLQKKGYDIE		147
:				
seq2	121	LIQEFYYYYALTKTVEGEQALTYLQERGFTHALIKERGIGFAPDSSHCHDFLQKKGYDIE		180
seq1	148	LAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAQGRIVGYSGRITYTGQEPKYLNSPETPIF		207
:				
seq2	181	LAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAQGRIVGYSGRITYTGQEPKYLNSPETPIF		240
seq1	208	QKRKLLYNLDKARKSIRKLDEIVLLEGFMDVIKSDTAGLKNVVATMGTQLSDEHITFIRK		267
:				
seq2	241	QKRKLLYNLDKARKSIRKLDEIVLLEGFMDVIKSDTAGLKNVVATMGTQLSDEHITFIRK		300
seq1	268	LTSNITLMFDGDFPGSEATLKTGQHLLQQGLNVFVIQLPSGMHPDEYIGKYGNDAFTTFV		327
:				
seq2	301	LTSNITLMFDGDFAGSEATLKTGQNLQQGLNVFVIQLPSGMDPDEYIGKYGNDAFTAFAV		360
seq1	328	KNHKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQQKAINDVAPFFNVS		387
:				
seq2	361	KNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQQKALNDVAPFFNVS		420
seq1	388	PEQLANEIQFNQAPANYYPEDEYGGYDEYGGYIEPEPIGMAQFDNLSRREKAERAFLKHL		447
:				
seq2	421	PEQLANEIQFNQAPANYYPE-----DEYGGYIEPEPIGMAQFDNLSRQEKERAERAFLKHL		474
seq1	448	MRDKDTFLNYYESVDKDNFTNQHFQYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLI		507
:				
seq2	475	MRDKDTFLNYYESVDKDNFTNQHFQYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLI		534
seq1	508	SLEQYNLNGEPYENEIDYVNVINEKGQETIESLNHKLREATRIGDVELQKYYLQQIVAK		567
:				
seq2	535	SLEQYNLNDPEYENEIDYVNVINEKGQETIESLNHKLREATRIGDVELQKYYLQQIVAK		594
seq1	568	NKERM	572	
:				
seq2	595	NKERM	599	

APPENDIX II

Optimal global alignment

Sequence 1

>US 10/025,222 (amino acids 1-34 of SEQ ID NO:2)
(34 letters)

Sequence 2

>Lynn Doucette-Stamm (US 6,380,370) (amino acids 1-34 of SEQ ID
NO:3636) (34 letters)

Substitution matrix: blosum62

Gap penalty: - (11 + 1 * (gap length))

Score: 157

Identical: 31/34 (91%), Similar: 34/34 (100%)

seq1	1	LRIDQSIINEIKDKTDILDLVSEYVKLEKRGRNY	34
		: : :	
seq2	1	LRIDQSVIDEIKNKTDILDLVSEYVKLEKRGRNY	34